

SEQUENCE LISTING

<110> Novartis AG

<120> Three-Dimensional Structure of the Catalytic Domain of ZAP-70 Protein Tyrosine Kinase, Methods and Use Thereof

<130> 4-32688

<160> 6

<170> PatentIn version 3.0

<210> 1

<211> 619

<212> PRT

<213> human

<400> 1

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
1 5 10 15

Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
20 25 30

Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
35 40 45

Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
50 55 60

Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
65 70 75 80

Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
85 90 95

Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
100 105 110

Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg

115		120		125
Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser				
130		135		140
Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg				
145		150		155
				160
Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys				
		165		170
				175
Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg				
		180		185
				190
Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val				
		195		200
				205
Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro				
		210		215
				220
Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys				
		225		230
				235
				240
Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn				
		245		250
				255
Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala				
		260		265
				270
His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn				
		275		280
				285
Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys				
		290		295
				300
Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser				
		305		310
				315
				320
Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn				
		325		330
				335
Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val				
		340		345
				350
Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile				
		355		360
				365
Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met				
		370		375
				380

Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg
 385 390 395 400
 Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met
 405 410 415
 Ala Gly Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu
 420 425 430
 Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly
 435 440 445
 Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala
 450 455 460
 Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe
 465 470 475 480
 Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg
 485 490 495
 Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn
 500 505 510
 Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr
 515 520 525
 Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys
 530 535 540
 Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys
 545 550 555 560
 Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp
 565 570 575
 Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg
 580 585 590
 Met Arg Ala Cys Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro
 595 600 605
 Gly Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala
 610 615

<210> 2

<211> 322

<212> PRT

<213> human

<400> 2

```

Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met Pro Met Asp Thr Ser
1           5           10           15
Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu Leu Lys Asp Lys Lys
          20           25           30
Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala Asp Ile Glu Leu Gly
          35           40           45
Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val Tyr Arg Met Arg Lys
          50           55           60
Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys Gln Gly Thr Glu Lys
65           70           75           80
Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln Ile Met His Gln Leu
          85           90           95
Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val Cys Gln Ala Glu Ala
          100          105          110
Leu Met Leu Val Met Glu Met Ala Gly Gly Gly Pro Leu His Lys Phe
          115          120          125
Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser Asn Val Ala Glu Leu
          130          135          140
Leu His Gln Val Ser Met Gly Met Lys Tyr Leu Glu Glu Lys Asn Phe
145          150          155          160
Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Val Asn Arg His
          165          170          175
Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys Ala Leu Gly Ala Asp
          180          185          190
Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys Trp Pro Leu Lys Trp
          195          200          205

```

Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe Ser Ser Arg Ser Asp
 210 215 220
 Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala Leu Ser Tyr Gly Gln
 225 230 235 240
 Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val Met Ala Phe Ile Glu
 245 250 255
 Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys Pro Pro Glu Leu Tyr
 260 265 270
 Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp Glu Asp Arg Pro Asp
 275 280 285
 Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys Tyr Tyr Ser Leu Ala
 290 295 300
 Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln Lys Ala Glu Ala Ala
 305 310 315 320

Cys Ala

<210> 3

<211> 74

<212> DNA

<213> unknown

<400> 3

cagatggata caccctgag ccagcactgg aagttctggt ccaggggccc cgcataacgt
 ccccagacaa accg

<210> 4

<211> 20

<212> DNA

<213> unknown

<400> 4
acaacgcacagaatctagcg

<210> 5

<211> 74

<212> DNA

<213> unknown

<400> 5
cacactccca gccacccat ccacgctgga agttctgttc caggggccct tgactcatcc
tcagagacga atcg

<210> 6

<211> 57

<212> DNA

<213> unknown

<400> 6
gctcgaattc tcaatgatga tgatgatgat gggcacaggc agcctcagcc ttctgtg